L2: Entry 42 of 48 File: USPT Feb 23, 1999

DOCUMENT-IDENTIFIER: US 5874479 A
TITLE: Therapeutic permeation enhanced-wound healing compositions and methods for preparing and using same

CLAIMS:

31. The augmented permeation enhanced-wound healing composition according to claim 19, wherein the medicament useful for treating wounds is a transforming growth factor selected from the group consisting of Type 1 TGF-beta, Type 2 TGF-beta, Type 3 TGF-beta, Type 4 TGF-beta, and Type 5 TGF-beta.

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Thursday, April 07, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND	
☐	L1	lefty-a.ti,ab,clm.	0
☐	L2	leftya.ti,ab,clm.	1
☐	L3	endometrial near bleeding-associated near factor	92
☐	L4	(leftya or lefty-a) near protein	2
☐	L5	(leftya or lefty-a) near protein	1
☐	L6	(leftya or lefty-a) near protein	1
☐	L7	left-right near determination	12
☐	L8	transformaing near growth near factor near (b4 or b-4 or beta4 or beta-4)	0
☐	L9	transforming near growth near factor near (b4 or b-4 or beta4 or beta-4)	2
☐	L10	transforming near growth near factor-(b4 or b-4 or beta4 or beta-4)	551
☐	L11	transforming near growth near factor(b4 or b-4 or beta4 or beta-4)	551
☐	L12	tfg near(b4 or b-4 or beta4 or beta-4)	0
☐	L13	tfg near (b4 or b-4 or beta4 or beta-4)	0
☐	L14	tgf near (b4 or b-4 or beta4 or beta-4)	13
☐	L15	tgfb4 or tgf-b4 or tgf-b-4 or tgf-beta4 or tgf-beta-4	18
☐	L16	tgf-beta near 4	152
☐	L17	L16 not l15 not l14 not l9	150

END OF SEARCH HISTORY

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Thursday, April 07, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND	
☐	L1	(tgfbeta or tgfb or tgf-beta or tgf-b) near5 4	595
☐	L2	L1.clm.	48
☐	L3	tgfb4 or tgfb-4	8
☐	L4	5808007.pn.	2
☐	L5	l4 and kit	0
☐	L6	l4 and (saline or water or purified or pbs or buffer or carrier or diluent or solute)	1

END OF SEARCH HISTORY

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Thursday, April 07, 2005

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND		
☐	L1	(tgfbeta or tgfb or tgf-beta or tgf-b) near5 4	595
☐	L2	L1.clm.	48
☐	L3	tgfb4 or tgfb-4	8

END OF SEARCH HISTORY

Generate Collection | Print

Search Results - Record(s) 1 through 8 of 8 returned.

1. 20050031643. 18 Jun 04. 10 Feb 05. Microorganisms for therapy. Szalay, Aladar A., et al. 424/199.1; 435/235.1 A61K039/12 C12N007/00.

2. 20030050242. 08 Feb 02. 13 Mar 03. Protein polymerization inhibitors and methods of use. Vahlne, Anders. 514/12; 514/18 A61K038/17 A61K038/06.

3. 20030032047. 26 Jul 02. 13 Feb 03. Method for diagnosing selected adenocarcinomas. Tabibzadeh, Siamak. 435/6; C12Q001/68 G01N033/53.

4. 20030031681. 13 Nov 01. 13 Feb 03. Combined growth factor-deleted and thymidine kinase-deleted vaccinia virus vector. McCart, J. Andrea, et al. 424/186.1; 435/235.1 435/456 A61K039/12 C12N015/863 C12N007/00.

5. 6683156. 16 Mar 00; 27 Jan 04. Method for diagnosing selected adenocarcinomas. Tabibzadeh; Siamak. 530/350; 530/351 530/399 536/23.1 536/23.5. C07K017/00 C07H021/04.

6. 6294662. 29 Jun 99; 25 Sep 01. Nucleic acids encoding an endometrial bleeding associated factor (ebaf). Tabibzadeh; Siamak. 536/23.5; 435/6 536/23.1 536/24.31 536/24.33. C07H021/04 C12Q001/68.

7. 5916751. 27 Aug 97; 29 Jun 99. Method for the diagnosis of selected adenocarcinomas. Tabibzadeh; Siamak, et al. 435/6; 435/7.23 436/64 436/813. G01N033/574 G01N033/48 C12Q001/68.

8. US 5916751A. Detecting serous or mucinous colon/ovarian adenocarcinomas and testicular adenocarcinoma by assaying for elevated expression of a gene. KOTHAPALLI, R, et al. C12Q001/68 G01N033/48 G01N033/574.

Generate Collection | Print

Terms	Documents
tgfb4 or tgfb-4	8

Prev Page Next Page Go to Doc#

6747004. 28 Apr 00; 08 Jun 04. Method for inducing growth and enhancing survival of nervous tissue. Tabibzadeh; Siamak. 514/12; 435/375 514/1 514/2 514/44. A61K038/00 A01N061/00 A01N037/18 C12N005/00.

☐ 2. 6683156. 16 Mar 00; 27 Jan 04. Method for diagnosing selected adenocarcinomas. Tabibzadeh; Siamak. 530/350; 530/351 530/399 536/23.1 536/23.5. C07K017/00 C07H021/04.

☐ 3. 6649588. 05 Oct 00; 18 Nov 03. Inhibition of TGF-.beta. and uses thereof. Tabibzadeh; Siamak, et al. 514/2; 514/21 514/899 530/350. A61K038/00 A01N025/00 C07K017/00.

☐ 4. 6294662. 29 Jun 99; 25 Sep 01. Nucleic acids encoding an endometrial bleeding associated factor (ebaf). Tabibzadeh; Siamak. 536/23.5; 435/6 536/23.1 536/24.31 536/24.33. C07H021/04 C12Q001/68.

☐ 5. 5916751. 27 Aug 97; 29 Jun 99. Method for the diagnosis of selected adenocarcinomas. Tabibzadeh; Siamak, et al. 435/6; 435/7.23 436/64 436/813. G01N033/574 G01N033/48 C12Q001/68.

☐ 6. 5338164. 28 May 93; 16 Aug 94. Positive displacement micropump. Sutton; Robert F., et al. 417/413.2;. F04B017/00.

☐ 7. 5171432. 05 Mar 91; 15 Dec 92. Liquid and particle separator. Tabibzadeh; Manouchehr. 210/94; 210/256 210/298 210/299 210/416.1. B01D029/64.

patients, 98 also had elevated CEA levels. Hence the rate of false negatives for the test was 41%, and the rate of false-positive results was 16%. (Moertel, C., et al. An Evaluation of the Carcinoembryonic Antigen (CEA) Test for monitoring Patients with resected Colon Cancer. JAMA 270(8):954 (1993).

Brief Summary Text (10):
In concluding their study, the authors questioned the efficacy of the CEA Test. In support of this conclusion, they explained that, based on their data, the maximum anticipated gain from CEA monitoring would probably be a small number of lives saved (less than 1% of patients monitored) after resection and hepatic metastasis. In addition, the authors specifically stated, "Since the most defensible objective of CEA monitoring is detection of potentially resectable hepatic metastasis, it would also seem appropriate to consider alternative strategies that might fulfill this objective in a more sensitive, specific, and cost-effective manner." (Id)

Brief Summary Text (11):
Another method used to screen for colon cancer is to have the patient undergo a periodic sigmoidoscopic examination. The use of this screening test in a particular patient is dependent upon the age of the patient and whether he or she is a member of a high-risk population. Research on this screening technique has concluded this method to be the best known screening method for colon cancer presently available (see Selby, J. Sigmoidoscopy in the Periodic Health Examination of Asymptomatic Adults JAMA (1989) 261(4):595)

Brief Summary Text (12):
However, researchers have also acknowledged that this screening method contains inherent limitations. For example, the high cost for the specialized instruments required to perform this screening test, and the special training required in the operation of the instruments in order to perform the procedure safely are acknowledged. Moreover, general patient discomfort while undergoing this screening is believed to be one of the obstacles in providing mass screening for the general population. Finally, health professionals acknowledge that there is a very slight risk of perforating a patient's colon while undergoing the procedure. Consequently, applicants believe a simple, cost effective screening test for colon cancer is needed.

Brief Summary Text (26):
Yet still another object of the present invention is to provide a blood test for adenocarcinomas of the testis, and mucinous adenocarcinomas of the colon and ovaries. As stated above, only 6 organs are presently known to express the ebaf gene constitutively. Applicants believe this constitutive expression results in a basal level of expression of the ebaf gene in the blood. However, if increased levels of expression of the ebaf gene are detected in the blood of a human relative to the basal level, they indicate the presence of an adenocarcinoma of the testis, or a mucinous adenocarcinoma of the colon or ovary. For example, if increased levels of expression of the ebaf gene are detected in a blood sample from a human male, such levels are indicative of an adenocarcinoma of the testis or a mucinous adenocarcinoma of the colon. If increased levels of expression of the ebaf gene are detected in a sample of blood taken from a female after her period, then such increased levels may be indicative of the presence of a mucinous adenocarcinoma in the colon or ovaries, provided the female does not suffer from abnormal uterine bleeding.

Detailed Description Text (11):
Squamous cell carcinomas and non-epithelial tumors for the expression were also examined for expression of the ebaf gene. The same Northern Blot protocol as explained above was also used for these tumors. The results of these tests are shown in Tables 3 and 4, respectively.

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UniProtKB/Swiss-Prot entry O00292

Entry information

Entry name	**TGFB4_HUMAN**
Primary accession number	**O00292**
Secondary accession numbers	O75611 Q8NBQ9
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 47, May 2005

Name and origin of the protein

Protein name	**Transforming growth factor beta 4 [Precursor]**
Synonyms	**TGF-beta 4** **Endometrial bleeding-associated factor** **Left-right determination factor A** **Lefty-A protein**
Gene name	**Name: EBAF** Synonyms: LEFTA, LEFTYA, TGFB4
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

References

[1] NUCLEOTIDE SEQUENCE.
TISSUE=Placenta;
MEDLINE=97298127;PubMed=9153275 [NCBI, ExPASy, EBI, Israel, Japan]
Kothapalli R., Buyuksal I., Wu S.-Q., Chegini N., Tabibzadeh S.;
"Detection of ebaf, a novel human gene of the transforming growth factor beta superfamily association of gene expression with endometrial bleeding.";
J. Clin. Invest. 99:2342-2350(1997).

[2] NUCLEOTIDE SEQUENCE, AND VARIANT L-R AXIS MALFORMATIONS ASN-342.
TISSUE=Placenta;
MEDLINE=99162193;PubMed=10053005 [NCBI, ExPASy, EBI, Israel, Japan]
Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G., Casey B.;
"Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left-right axis development.";
Am. J. Hum. Genet. 64:712-721(1999).

[3] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
DOI=10.1038/ng1285;PubMed=14702039 [NCBI, ExPASy, EBI, Israel, Japan]
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., [redacted], Sugano S.;
"Complete sequencing and characterization of 21,243 full-length human cDNAs.";
Nat. Genet. 36:40-45(2004).

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Ovary;
DOI=10.1073/pnas.242603899;MEDLINE=22388257;PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., [redacted], Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Comments

- ***FUNCTION***: Required for left-right (L-R) asymmetry determination of organ systems in mammals. May play a role in endometrial bleeding.
- ***SUBCELLULAR LOCATION***: Secreted.
- ***TISSUE SPECIFICITY***: Mesenchymal cells of the endometrial stroma.
- ***DEVELOPMENTAL STAGE***: Transiently expressed before and during menstrual bleeding.
- ***PTM***: The processing of the protein may also occur at the second R-X-X-R site located at AA 132-135. Processing appears to be regulated in a cell-type specific manner.
- ***DISEASE***: Defects in EBAF are the cause of left-right axis malformations (L-R axis malformation) [MIM:601877]. The defect includes left pulmonary isomerism, with cardiac anomalies characterized by complete atrioventricular canal defect and hypoplastic left ventricle, and interrupted inferior vena cava.
- ***SIMILARITY***: Belongs to the TGF-beta family.
- ***CAUTION***: Ref.1 authors have revised their sequence to agree with the one shown in this entry, but have not submitted the revised DNA sequence.

Copyright

Cross-references

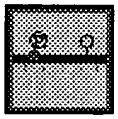
EMBL	U81523; AAB53269.1; ALT_SEQ. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081511; AAC32600.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081508; AAC32600.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081509; AAC32600.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081510; AAC32600.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081513; AAD48145.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AK075344; BAC11556.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	BC035718; AAH35718.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P10600; 1TGJ. [HSSP ENTRY / PDB]
Ensembl	ENSG00000143768; Homo sapiens. [Contig view]
Genew	HGNC:3122; EBAF.
CleanEx	HGNC:3122; EBAF.

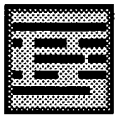
GeneCards	EBAF.
GeneLynx	EBAF; Homo sapiens.
GenAtlas	EBAF.
H-InvDB	HIX0001640; -.
MIM	601877 [NCBI / EBI].
GO	GO:0007275; Biological process: development *(traceable author statement).* GO:0007309; Biological process: oocyte axis determination *(traceable author statement).* GO:0007179; Biological process: transforming growth factor beta receptor signaling pathway *(traceable author statement).* QuickGo view.
SOURCE	EBAF; Homo sapiens.
InterPro	IPR001839; TGFb. IPR001111; TGFb_N. Graphical view of domain structure.
Pfam	PF00019; TGF_beta; 1. PF00688; TGFb_propeptide; 1. Pfam graphical view of domain structure.
PRINTS	PR01427; TGFBETA4.
ProDom	PD000357; TGFb; 1. [Domain structure / List of seq. sharing at least 1 domain]
PROSITE	PS00250; TGF_BETA_1; 1.
HOVERGEN	[Family / Alignment / Tree]
BLOCKS	O00292.
ProtoNet	O00292.
ProtoMap	O00292.
PRESAGE	O00292.
DIP	O00292.
ModBase	O00292.
SMR	O00292; 63A416CAE30F7A39.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Cytokine; **Developmental protein**; **Disease mutation**; **Glycoprotein**; **Growth factor**; **Multigene family**; **Signal**.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description	FTId
SIGNAL	1	21	21	*Potential.*	
PROPEP	22	76	55	Or 135 *(Potential)*.	
CHAIN	77	366	290	Transforming growth factor beta 4.	

DISULFID	251	264		*By similarity.*
DISULFID	263	316		*By similarity.*
DISULFID	293	351		*By similarity.*
DISULFID	297	353		*By similarity.*
CARBOHYD	158	158		N-linked (GlcNAc...) *(Potential).*
VARIANT	342	342	1	S -> N (in L-R axis malformations). VAR_010385
CONFLICT	183	183		A -> P (in Ref. 3).

Sequence information

Length: **366 AA** [This is the length of the unprocessed precursor]

Molecular weight: **40920 Da** [This is the MW of the unprocessed precursor]

CRC64: **63A416CAE30F7A39** [This is a checksum on the sequence]

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MWPLWLCWAL WVLPLAGPGA ALTEEQLLGS LLRQLQLSEV PVLDRADMEK LVIPAHVRAQ

        70         80         90        100        110        120
YVVLLRRSHG DRSRGKRFSQ SFREVAGRFL ASEASTHLLV FGMEQRLPPN SELVQAVLRL

       130        140        150        160        170        180
FQEPVPKAAL HRHGRLSPRS AQARVTVEWL RVRDDGSNRT SLIDSRLVSV HESGWKAFDV

       190        200        210        220        230        240
TEAVNFWQQL SRPRQPLLLQ VSVQREHLGP LASGAHKLVR FASQGAPAGL GEPQLELHTL

       250        260        270        280        290        300
DLRDYGAQGD CDPEAPMTEG TRCCRQEMYI DLQGMKWAKN WVLEPPGFLA YECVGTCQQP

       310        320        330        340        350        360
PEALAFNWPF LGPRQCIASE TASLPMIVSI KEGGRTRPQV VSLPNMRVQK CSCASDGALV

PRRLQP
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O00292 in FASTA format

View entry in original Swiss-Prot format
View entry in raw text format (no links)
Report form for errors/updates in this Swiss-Prot entry

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

UniProtKB/Swiss-Prot entry Q64280

Entry information

Entry name	**TGFB4_MOUSE**
Primary accession number	**Q64280**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 47, May 2005

Name and origin of the protein

Protein name	**Transforming growth factor beta 4 [Precursor]**
Synonyms	**TGF-beta 4** **Lefty protein** **Lefty-1 protein** **STRA3 protein**
Gene name	**Name: Ebaf** Synonyms: Lefty, Lefty1, Stra3, Tgfb4
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

References

[1] NUCLEOTIDE SEQUENCE.
DOI=10.1038/381151a0;MEDLINE=96202359;PubMed=8610011 [NCBI, ExPASy, EBI, Israel, Japan]
Meno C., Saijoh Y., Fujii H., Ikeda M., Yokoyama T., Yokoyama M., Toyoda Y., Hamada H.;
"Left-right asymmetric expression of the TGF beta-family member lefty in mouse embryos.";
Nature 381:151-155(1996).

[2] NUCLEOTIDE SEQUENCE.
Bouillet P.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

[3] NUCLEOTIDE SEQUENCE.
MEDLINE=98156497;PubMed=9496783 [NCBI, ExPASy, EBI, Israel, Japan]
Oulad-Abdelghani M., Chazaud C., Bouillet P., Mattei M.-G., Dolle P., Chambon P.;
"Stra3/lefty, a retinoic acid-inducible novel member of the transforming growth factor-beta superfamily.";

Int. J. Dev. Biol. 42:23-32(1998).

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Embryonic stem cells;
DOI=10.1073/pnas.242603899;MEDLINE=22388257;PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., [redacted], Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5] FUNCTION.
DOI=10.1016/S0092-8674(00)81472-5;MEDLINE=98372436;PubMed=9708731 [NCBI, ExPASy, EBI, Israel, Japan]
Meno C., Shimono A., Saijoh Y., Yashiro K., Mochida K., Ohishi S., Noji S., Kondoh H., Hamada H.;
"Lefty-1 is required for left-right determination as a regulator of lefty-2 and nodal.";
Cell 94:287-297(1998).

Comments

- ***FUNCTION***: Required for left-right axis determination as a regulator of LEFTY2 and NODAL.
- ***SUBCELLULAR LOCATION***: Secreted.
- ***DEVELOPMENTAL STAGE***: By E8.0, expressed exclusively on the left side of developing embryos with expression predominantly in the prospective floor plate (PFP). Weak expression in the lateral-plate mesoderm (LPM).
- ***PTM***: The processing of the protein may also occur at the second R-X-X-R site located at AA 132-135. Processing appears to be regulated in a cell-type specific manner.
- ***SIMILARITY***: Belongs to the TGF-beta family.

Copyright

Cross-references

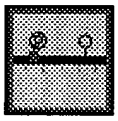
EMBL	D83921; BAA12121.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] Z73151; CAA97497.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AJ000082; CAA03909.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AJ000083; CAA03910.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] BC050221; AAH50221.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	S67507; S67507.
HSSP	P10600; 1TGJ. [HSSP ENTRY / PDB]
Ensembl	ENSMUSG00000038793; Mus musculus. [Contig view]
MGD	MGI:107405; Ebaf.
CleanEx	MGI:107405; Ebaf.
GeneLynx	Ebaf; Mus musculus.
GO	GO:0005615; Cellular component: extracellular space *(traceable author statement)*. QuickGo view.
SOURCE	Ebaf; Mus musculus.
InterPro	IPR001839; TGFb. IPR001111; TGFb_N.

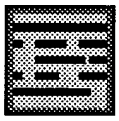
	Graphical view of domain structure.
Pfam	PF00019; TGF_beta; 1. PF00688; TGFb_propeptide; 1. Pfam graphical view of domain structure.
PRINTS	PR01427; TGFBETA4.
ProDom	PD000357; TGFb; 1. [Domain structure / List of seq. sharing at least 1 domain]
SMART	SM00204; TGFB; 1.
PROSITE	PS00250; TGF_BETA_1; 1.
HOVERGEN	[Family / Alignment / Tree]
BLOCKS	Q64280.
ProtoNet	Q64280.
ProtoMap	Q64280.
PRESAGE	Q64280.
DIP	Q64280.
ModBase	Q64280.
SMR	Q64280; 821DAE663C546B5F.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Cytokine; **Developmental protein**; **Glycoprotein**; **Growth factor**; **Signal**.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description
SIGNAL	1	21	21	*Potential.*
PROPEP	22	76	55	Or 135 *(Potential).*
CHAIN	77	368	292	Transforming growth factor beta 4.
DISULFID	253	266		*By similarity.*
DISULFID	265	318		*By similarity.*
DISULFID	295	353		*By similarity.*
DISULFID	299	355		*By similarity.*
CARBOHYD	158	158		N-linked (GlcNAc...) *(Potential).*

Sequence information

Length: **368 AA** [This is the length of the unprocessed precursor]

Molecular weight: **41498 Da** [This is the MW of the unprocessed precursor]

CRC64: **821DAE663C546B5F** [This is a checksum on the sequence]

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MPFLWLCWAL WALSLVSLRE ALTGEQILGS LLQQLQLDQP PVLDKADVEG MVIPSHVRTQ

        70         80         90        100        110        120
YVALLQHSHA SRSRGKRFSQ NLREVAGRFL VSETSTHLLV FGMEQRLPPN SELVQAVLRL

       130        140        150        160        170        180
FQEPVPRTAL RRQKRLSPHS ARARVTIEWL RFRDDGSNRT ALIDSRLVSI HESGWKAFDV
```

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       190         200         210         220         230         240
TEAVNFWQQL SRPRQPLLLQ VSVQREHLGP GTWSSHKLVR FAAQGTPDGK GQGEPQLELH

       250         260         270         280         290         300
TLDLKDYGAQ GNCDPEAPVT EGTRCCRQEM YLDLQGMKWA ENWILEPPGF LTYECVGSCL

       310         320         330         340         350         360
QLPESLTSRW PFLGPRQCVA SEMTSLPMIV SVKEGGRTRP QVVSLPNMRV QTCSCASDGA

LIPRRLQP
```

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Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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L6: Entry 1 of 1 File: USPT Nov 18, 2003

DOCUMENT-IDENTIFIER: US 6649588 B1
TITLE: Inhibition of TGF-.beta. and uses thereof

Detailed Description Text (2):
The present invention provides a method for inhibiting TGF-.beta. activity, comprising contacting tissue expressing TGF-.beta. with an amount of ebaf effective to inhibit the activity of TGF-.beta.. Unless otherwise indicated, "ebaf" includes both an ebaf (lefty-A) protein and an "ebaf analogue" As used herein, ebaf protein has the amino acid sequence set forth in FIG. 2. An "ebaf analogue" is a functional variant of the ebaf protein, having ebaf-protein biological activity, that has 80% or greater (preferably, 90% or greater) amino-acid-sequence homology with the ebaf protein, as well as a fragment of the ebaf protein having ebaf-protein biological activity. As used herein, the term "ebaf-protein biological activity" refers to protein activity which inhibits activity of TGF-.beta., as disclosed below. Additionally, the term "ebaf analogue", as defined herein, includes peptides related to ebaf that exert similar ebaf-protein biological activity, particularly lefty-B, lefty-1, and lefty-2 proteins, and preferably lefty-B. Ebaf may be produced synthetically or recombinantly, or may be isolated from native cells; however, it is preferably produced recombinantly, using cDNA encoding ebaf (FIG. 2), along with conventional techniques.

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CASDGALVRRLGTRP